

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 21:05:24 ; Search time 1445 Seconds

(without alignments)
1008.715 Million cell updates/sec

Title: US-09-910-757-1

Perfect score: 90

Sequence: 1 gggagagcgccggtggtgcg.....cggtgccccgcgcaggtcg 90

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	90	100.0	300	9	AU098678
2	90	100.0	350	12	BE831859
3	90	100.0	447	14	BM694414
4	90	100.0	571	13	BI547746
5	90	100.0	635	13	BI547550
6	90	100.0	653	9	AL042549

7	90	100.0	657	12	BG722295
8	90	100.0	677	13	BI559391
9	90	100.0	679	13	BI597041
10	90	100.0	685	12	BG719125
11	90	100.0	701	13	BM172428
12	90	100.0	705	13	BI545908
13	90	100.0	715	12	BG709029
14	90	100.0	716	13	BI544366
15	90	100.0	734	12	BG704185
16	90	100.0	776	12	BG764788
17	90	100.0	785	13	BI761515
18	90	100.0	829	13	BI561536
19	90	100.0	867	12	BF315675
20	90	100.0	869	9	AL550975
21	90	100.0	891	14	BQ897731
22	90	100.0	895	12	BF204878
23	90	100.0	900	14	BQ440126
24	90	100.0	920	9	AL543516
25	90	100.0	929	12	BF979775
26	90	100.0	931	14	BQ688437
27	90	100.0	944	9	AL550425
28	90	100.0	969	14	BQ880712
29	90	100.0	1031	9	AL533088
30	90	100.0	1494	14	BQ706464
31	88.8	98.7	895	9	AL537562
32	88.8	98.7	897	9	AL518480
33	88.4	98.2	641	13	BI545987
34	88.4	98.2	699	9	AU137092
35	88.4	98.2	821	9	AL557346
36	88	97.8	612	9	AU128077
37	88	97.8	911	9	AL532648
38	87.4	97.1	639	14	BQ807996
39	86	95.6	862	12	BE735858
40	85.4	94.9	772	12	BG701016
41	85.2	94.7	1050	14	BQ882754
42	79	87.8	712	12	BG720447
43	79	87.8	728	13	BI601746
44	78	86.7	723	12	BE867517
45	77.4	86.0	154	9	AU077057

ALIGNMENTS

RESULT 1
AU098678
LOCUS
DEFINITION
AU098678 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
COL09158 similar to Human mRNA for amyloid A4 precursor of
Alzheimer's disease, mRNA sequence.
ACCESSION
AU098678
VERSION
AU098678.1 GI:13549807
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 300)
Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata
, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo
, K., Suyama, A. and Sugano, S.
'S. Construction and characterization of a full length-enriched and
enriched and 5'-end enriched cDNA libraries constructed by
Oligo-capping method
Unpublished (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
, S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES	source	Location/Qualifiers
BASE COUNT	50 a	86 c 112 g 52 t
ORIGIN		1. .300 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="COL09158" /clone_lib="Sugano Homo sapiens cDNA library" /note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"
Query Match	100.0%;	Score 90; DB 9; Length 300;
Best Local Similarity	100.0%;	Pred. No. 6.2e-13;
Matches	90; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	GGGAGACGGCGGGTGGCGGGCGGCGGAGCAAGGACGGCGGATCCACTCCGACA 60
Db	56	GGGAGACGGCGGGTGGCGGGCGGCGGAGCAAGGACGGCGGATCCACTCCGACA 115
QY	61	GCAGCGACTCGGTGCCCGCGCAGGGTCG 90
Db	116	GCAGCGACTCGGTGCCCGCGCAGGGTCG 145
RESULT 2		
BE831859/c		
LOCUS		350 bp mRNA linear EST 22-SEP-2000
DEFINITION		RC6-MT0061-310700-021-G04 MT0061 Homo sapiens cDNA, mRNA sequence.
ACCESSION		BE831859
VERSION		BE831859.1 GI:10264237
KEYWORDS		EST.
SOURCE		human.
ORGANISM		Homo sapiens
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS		Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE		Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE		20202663
COMMENT		Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RC6-MT0061-310700-021-G04&t3=2000-07-31&t4=1) Seq primer: puc 18 forward High quality sequence stop: 345.
FEATURES		Location/Qualifiers
source		1. .350 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="MT0061" /dev_stage="Adult" /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

Qy 61 GCAGCGCACTCGGTGCCCGCGCAGGGTCG 90

SOURCE
ORGANISM human.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 1 (bases 1 to 653) Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Blum H
 MIPS
 Am Klopferspitz 18a D-82152 Martinsried, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by LMU (Ludwig Maximilians University,
 Munich/Germany) within the CDNA sequencing consortium of the German
 Genome Project.
 No sl sequence available.
 This clone (DKFZp43I2421) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
 1..653
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="DKFZp43I2421"
 /clone_lib="434 (synonym: htes3)"
 /tissue_type="testis"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Vector: pSPort1; Site_1: NotI; Site_2: SalI"
BASE COUNT
ORIGIN
 150 a 183 c 198 g 121 t
 Query Match 100.0%; Score 90; DB 9; Length 653;
 Best Local Similarity 100.0%; Pred. No. 7.1e-13;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGGAGACGGCGCGGTGGCGGGCGAGACGAGGAGCGGCGGATCCCACTCGCACA 60
 Db 46 GGGAGACGGCGCGGTGGCGGGCGAGACGAGGAGCGGCGGATCCCACTCGCACA 105
 Qy 61 GCAGCGCACTCGGTGCCCGCGCAGGTCG 90
 Db 106 GCAGCGCACTCGGTGCCCGCGCAGGTCG 135
RESULT 7
 BG722295 602693472F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4825960 5',
 LOCUS mRNA sequence.
DEFINITION BG722295.1 GI:14001482
ACCESSION BG722295
VERSION BG722295.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE 1 (bases 1 to 657)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: L1AM10739 row: o column: 17
 High quality sequence stop: 655.
FEATURES
source
 1..657
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4825960"
 /clone_lib="NIH_MGC_97"
 /lab_host="DH10B"
 /note="Organ: testis; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
 size-selected for average insert size 2.2 kb and
 normalized to ROT 5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIMH/NHGRI, National
 Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT
ORIGIN
 150 a 182 c 203 g 122 t
 Query Match 100.0%; Score 90; DB 12; Length 657;
 Best Local Similarity 100.0%; Pred. No. 7.1e-13;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGGAGACGGCGCGGTGGCGGGCGAGACGAGGAGCGGCGGATCCCACTCGCACA 60
 Db 64 GGGAGACGGCGCGGTGGCGGGCGAGACGAGGAGCGGCGGATCCCACTCGCACA 123
 Qy 61 GCAGCGCACTCGGTGCCCGCGCAGGTCG 90
 Db 124 GCAGCGCACTCGGTGCCCGCGCAGGTCG 153
RESULT 8
 BI559391 603253071F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5295369 5',
 LOCUS mRNA sequence.
DEFINITION BI559391
ACCESSION BI559391
VERSION BI559391.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM11747 row: n column: 18
 High quality sequence stop: 677.
FEATURES
source
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5295369"
 /clone_lib="NIH_MGC_97"
 /lab_host="DH10B"
 /note="Organ: testis; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
 size-selected for average insert size 2.2 kb and


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/tissue_type="hippocampus"
/lab_host="nug102"
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BASE COUNT

BASE COUNT

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Matches	90; Conservative	0;	Mismatches	0;	Indels
Gaps	0;				
QY	1	GGGAGACGGCGGTGGCGGCCGGGCAGAGCAAGACGCGCGGATCCACTCGCAC	60		
Db	64	GGGAGACGGCGGTGGCGGCCGGGCAGAGCAAGACGCGCGGATCCACTCGCAC			
QY	61	GCAGCGCACTCGGTGCCCGCGCAGGGTCG	90		
Db	124	GCAGCGCACTCGGTGCCCGCGCAGGGTCG	153		

Search completed: July 12, 2003, 21:58:09
Job time : 1450 secs